



## SEQUENCE LISTING

<110> Oklahoma Medical Research Foundation  
Sauer, Brian Lee  
Rufer, Andreas Walter

<120> Method for Selecting Recombinase Variants with Altered Specificity

<130> OMRF 178

<140> 09/544,045

<141> 2000-04-06

<150> 60/127,977

<151> 1999-04-06

<160> 68

<170> PatentIn version 3.1

<210> 1

<211> 343

<212> PRT

<213> Artificial Sequence

<220>

<223> Cre

<400> 1

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Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg  
20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val  
35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe  
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala  
65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn  
85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala  
100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly  
 115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln  
 130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn  
 145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu  
 165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg  
 180 185 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly  
 195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp  
 210 215 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys  
 225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu  
 245 250 255

Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile  
 260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly  
 275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val  
 290 295 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile  
 305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val  
 325 330 335

Arg Leu Leu Glu Asp Gly Asp  
340

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<220>  
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<220>  
<221> misc\_feature  
<222> (1)..(3)  
<223> N at positions 1-3 can be A, T, G, or C.

<220>  
<221> misc\_feature  
<222> (6)..(7)  
<223> N at positions 6 and 7 can be A, T, G, or C.

<400> 2  
nnnacnncgt ata

13

<210> 3  
<211> 34  
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<213> artificial sequence

<220>  
<223> variant lox sites

<220>  
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<223> N at positions 1-3 can be A, G, C, or T

<220>  
<221> misc\_feature  
<222> (6)..(7)  
<223> N at positions 6 and 7 can be A, T, G, C,

<220>  
<221> misc\_feature  
<222> (14)..(21)  
<223> N at positions 14-21 can A, G, T, or C

<220>  
<221> misc\_feature  
<222> (28)..(29)

<223> N at postions 28 and 29 can be A, T, G, or C

<220>

<221> misc\_feature

<222> (32)..(34)

<223> N at postiions 32-34 can be A, T, G, or C

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nnnacnncgt atannnnnnn ntatacgngg tnnn

34

<210> 4

<211> 33

<212> DNA

<213> artificial sequence

<220>

<223> variant lox sites

<400> 4

gatacaacgt atataccttt ctatacgttg tat

33

<210> 5

<211> 34

<212> DNA

<213> artificial sequence

<220>

<223> Specific and non-specific sequences for Cre recombinase

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<223> N at postions 1-3 can be A, T, G, or C

<220>

<221> misc\_feature

<222> (14)..(21)

<223> N at positions 14-21 can be A, T, C, or G

<220>

<221> misc\_feature

<222> (32)..(34)

<223> N at positions 32-34 can be A, T, G, or C

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<210> 6

<211> 8

<212> PRT  
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<210> 7  
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<220>  
<223> primer

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34

<210> 8  
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29

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<220>  
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31

<210> 10  
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<220>  
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ataagcggcc gctgagcttg gctgttttgg cgg

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<400> 11  
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36

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<220>  
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<400> 13  
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<220>  
<223> primer

<400> 14  
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<223> primer  
  
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 <223> primer  
  
 <400> 17  
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 <223> primer  
  
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 <223> primer  
  
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 <212> DNA  
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 gctatcaact cgcgccctgg gagggatttt tgaagcaact catcg 45  
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 <400> 23  
 gagttgcttc aaaaatccct cccagggcgc gagttgatag ctggc 45  
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 <400> 24  
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<210> 25  
<211> 45  
<212> DNA  
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<220>  
<223> primer

<400> 25  
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45

<210> 26  
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<220>  
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<222> (17)..(25)  
<223> N at positions 17-25 can be A, T, G, or C

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<220>  
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<222> (17)..(25)  
<223> N at positions 17-25 can be A, T, G, or C

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<210> 28  
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<220>  
<223> wtCre

<400> 28

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ggttcgcaag aacctgatgg acatgttcag ggatcgccag gcgttttctg agcatacctg	180
gaaaatgctt ctgtccgttt gccggtcgtg ggcggcatgg tgcaagttga ataaccggaa	240
atggtttccc gcagaacctg aagatgttcg cgattatctt ctatatcttc aggcgcgcgg	300
tctggcagta aaaactatcc agcaacattt gggccagcta aacatgcttc atcgtcggtc	360
cgggctgcc aagaccaagt acagcaatgc tgtttcactg gttatgcggc ggatccgaaa	420
agaaaacggt gatgccggtg aacgtgcaaa acaggctcta gcgttcgaac gcactgattt	480
cgaccagggt cgttcactca tggaaaatag cgatcgctgc caggatatac gtaatctggc	540
atttctgggg attgcttata acaccctgtt acgtatagcc gaaattgcc aagatcagggt	600
taaagatata tcacgtactg acggtgggag aatgttaatc catattggca gaacgaaaac	660
gctgggttagc accgcagggt tagagaaggc acttagcctg ggggtaacta aactggtcga	720
gcgatggatt tccgtctctg gtgtagctga tgatccgaat aactacctgt tttgccgggt	780
cagaaaaaat ggtgttgccg cgccatctgc caccagccag ctatcaactc gcgccctgga	840
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tggagtttca ataccggaga tcatgcaagc tgggtggctg accaatgtaa atattgtcat	1020
gaactatata cgtaacctgg atagtgaac aggggcaatg gtgcgcctgc tggaagatgg	1080
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tcagcctgat acagattaaa tcagaacgca ga	1172

<210> 29  
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<220>  
 <223> mxoxox1

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caatttactg accgtacacc aaaatttgcc tgcattacct gtcgatgcaa cgagtgatga	120
ggttcgcaag aacctgatgg ccatgttcag ggatcgccag gcgttttctg agcatacctg	180
gaaaatgctt ctgtccgttt gccggtcgtg ggcggcatgg tgcaagttga ataaccggaa	240

atggtttccc gcagaacctg aagatgttcg cgattatctt ctatatcttc aggcgcgcgg	300
tctggcagta aaaactatcc agcaacatth gggccagcta aacatgcttc atcgtcggtc	360
cgggctgcc aacccaagt acagcaatgc tgtttcactg gttatgcggc ggatccgaaa	420
agaaaacgtt gatgccggtg aacgtgcaaa acaggctcta gcgttcgaac gcaactgattt	480
cgaccagggt cgttcactca tggaaaatag cgatcgctgc caggatatac gtaactctggc	540
atttctgggg attgcttata acaccctgtt acgtatagcc gaaattgcca ggatcagggt	600
taaagatatc tcacgtacta acgggtgggag aatgttaatc catattggca gaacgaaaac	660
gctgggttagc accgcagggt tagagaaggc acttagtctg ggggtaacta aactggtcga	720
gcgatggatt tccatctctg gtgtagctga tgatccgaat aactacctgt tttgccgggt	780
cagaaaaaat ggtgttgccg cgccatctgc caccagccag ctatcaactc gcgccttggg	840
agggattttt gaagcaactc atcgattgat ttacggcgct aaggatgact ctggtcagag	900
atacctggcc tggctctggac acagtgcctg tgctggagcc gcgcgagata tggcccgcgc	960
tggagtttca ataccggaga tcatgcaagc tgggtggctgg accaatgtaa atattgtcat	1020
gaactatatc cgtaacctgg atagtgaac aggggcaatg gtgcgcctgc tggagatgg	1080
cgattagcca ttaacgcgta aatgataagc ttggctgttt tggcggatga gagaagattt	1140
tcagcctgat acagattaaa tcagaacgca ga	1172

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 <211> 1172  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> mxoxox2

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caatttactg accgtacacc aaaatttgcc tgcattacct gtcgatgcaa cgagtgatga	120
ggttcgcaag aacctgatgg acatgttcag ggatcgccag gcgttttctg agcatacctg	180
gaaaatgctt ctgtccgttt gccggctcgtg ggcggcatgg tgcaagttga ataaccggaa	240
atggtttccc gcagaacctg aagatgttcg cgattatctt ctatatcttc aggcgcgcgg	300
tctggcagta aaaactatcc agcaacatth gggccagcta aacatgcttc atcgtcggtc	360
cgggctgcc aacccaagt acagcaatgc tgtttcactg gttatgcggc ggatccgaaa	420

agaaaacgtt gatgccggtg aacgtgcaaa acaggctcta gcgttcggac gcactgattt	480
cgaccagggtt cgttcactca tggaaaatag cgatcgctgc caggatatac gtaatctggc	540
atttctgggg attgcttata acaccctgtt acgtatagcc gaaattgcca ggatcagggt	600
taaagatatc tcacgtactg acggtgggag aatgttaatc catattggca gaacgaaaac	660
gctgggttagc accgcagggt tagagaaggc acttagcctg ggggtaacta aactggtcga	720
gcgatggatt tccgtctctg gtgtagctga tgatccgaat aactacctgt tttgccgggt	780
cagaaaaaat ggtgttgccg cgccatctgc caccggccag ctatcaactc gcgccctggg	840
agggattttt gaagcaactc atcgattgat ttacggcgct aaggatgact ctggtcagag	900
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tggagtttca ataccggaga tcatgcaagc tgggtggctgg tccaatgtaa atattgtcat	1020
gaactatatc cgtaacctgg atagtgaac aggggcaatg gtgcgcctgc tggaagatgg	1080
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tcagcctgat acagattaaa tcagaacgca ga	1172

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 <223> mxoxox3

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ggttcgcaag aacctgatgg acatgttcag ggatcgccag gcgttttctg agcatacctg	180
gaaaatgctt ctgtccgttt gccggtcgtg ggcggcatgg tgcaagttga ataaccggaa	240
atggtttccc gcagaacctg aagatgttcg cgattatctt ctatatcttc aggcgcgcgg	300
tctggcagta aaaactatcc agcaacatctt gggccagcta aacatgcttc atcgtcggtc	360
cgggctgcca cgaccaagtg acagcaatgc tgtttcactg gttatgcggc ggatccgaaa	420
agaaaacgtt gatgccggtg aacgtgcaaa acaggctcta gcgttcgaac gcactgattt	480
cgaccagggtt cgttcactca tggaaaatag cgatcgctgc caggatatac gtaatctggc	540
atttctgggg attgcttata acaccctgtt acgtatagcc gaaattgcca ggatcagggt	600
taaagatatc tcacgtacta acggtgggag aatgttaatc catattagca gaacgaaaac	660

gctgggttagc accgcaggtg tagagaaggc acttagcctg ggggtaacta aactgggtcga	720
gcaatgggatt tccgtctctg gtgtagctga tgatccgaat aactacctgt tttgccgggt	780
cagaaaaaat ggtgttgccg cgccatctgc caccagccgg ctatcaactc gcgccctggg	840
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gaactatata cgtaacctgg atagtgaac aggggcaatg gtgcgcctgc tggaagatgg	1080
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tcagcctgat acagattaaa tcagaacgca ga	1172

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ggttcgcaag aacctgatgg acatgttcag ggatcgccag gcgttttctg agcatacctg	180
gaaaatgctt ctgtccgttt gccggtcgtg ggcggcatgg tgcaagttga ataaccggaa	240
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ataccaggcc tggctctggac acagtgcccg tgctcgagcc gcgcgagata tggcccgcgc	960
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gaactatatc cgtaacctgg atagtgaaac aggggcaatg gtgcgcctgc tggaagatgg	1080
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gaaaatgctt ctgtccgttt gccggtcgtg ggcggcatgg tgcaagttga ataaccggaa	240
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tctggcagta aaaactatcc agcaacatctt gggccagcta aacatgcttc atcgtcagtc	360
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cagaaaaaat ggtgttgccg cgccatctgc caccagccag ctatcaactc gcgccctggg	840
agggattttt gaagcaactc atcgattgat ttacggcgct aaggatgact ctggtcagag	900
atacctggcc tggctctggac acagtgcccg tgctcgagcc gcgcgagata tggcccgcgc	960
tggagtttca ataccggaga tcatgcaagc tggtagctgg tccaatgtaa atattgtcat	1020
gaactatatc cgtaacctgg atagtgaaac aggggcaatg gtgcgcctgc tggaagatgg	1080

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 ggttcgcaag aacctgatgg acatgttcag ggatcgccag gcgttttctg agcatacctg 180  
 gaaaatgctt ctgtccgttt gccggtcgtg ggcggcatgg tgcaagttga ataaccggaa 240  
 atggtttccc gcagaacctg aagatgttcg cgattatctt ctatatcttc aggcgcgcgg 300  
 tctggcagta aaaactatcc agcaacatctt gggccagcta aacatgcttc atcgtcggtc 360  
 cgggctgcca cgaccaagtg acagcaatgc tgtttcactg gttatgcggc ggatccgaaa 420  
 agaaaacgtt gatgccggtg aacgtgcaaa acaggctcta gcgttcgaac gcactgattt 480  
 cgaccagggtt cgttcactca tggaaaatag cgatcgctgc caggatatac gtaatctggc 540  
 atttctgggg attgcttata acacctgtt acgtatagcc gaaattgcca ggatcagggt 600  
 taaagatatc tcacgtactg acggtgggag aatgttaatc catattggca gaacgaaaac 660  
 gctgggttagc accgcagggtg tagagaaggc acttagcctg ggggtaacta aactggtcga 720  
 gcgatggatt tccgtctctg gtgtagctga tgatccgaat aactacctgt tttgccgggt 780  
 cagaaaaaat ggtgttgccg cgccatctgc caccagccag ctatcaactc gcgccctggg 840  
 agggattttt gaagcaactc atcgattgat ttacggcgct aaggatgact ctggtcagag 900  
 ataccaggcc tgggtctggac acagtgcccg tgtcggagcc gcgcgagata tggcccgcgc 960  
 tggagtttca ataccggaga tcatgcaagc tgggtggctg tccaatgtaa atattgtcat 1020  
 gaactatatc cgtaacctgg atagtgaaac aggggcaatg gtgcgcctgc tggaagatgg 1080  
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<210> 35

<211> 343  
<212> PRT  
<213> artificial sequence

<220>  
<223> mxoxox1

<400> 35

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val  
1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Ala Met Phe Arg  
20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val  
35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe  
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala  
65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn  
85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala  
100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly  
115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln  
130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn  
145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu  
165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asn Gly Gly Arg  
180 185 190



Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly  
195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp  
210 215 220

Ile Ser Ile Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys  
225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu  
245 250 255

Ser Thr Arg Ala Leu Gly Gly Ile Phe Glu Ala Thr His Arg Leu Ile  
260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly  
275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val  
290 295 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile  
305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val  
325 330 335

Arg Leu Leu Glu Asp Gly Asp  
340

<210> 36  
<211> 343  
<212> PRT  
<213> artificial sequence

<220>  
<223> mxoxox2

<400> 36

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val  
1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg  
20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val  
35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe  
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala  
65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn  
85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala  
100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly  
115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Gly Arg Thr Asp Phe Asp Gln  
130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn  
145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu  
165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg  
180 185 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly  
195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp  
210 215 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys  
225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Gly Gln Leu  
245 250 255

Ser Thr Arg Ala Leu Gly Gly Ile Phe Glu Ala Thr His Arg Leu Ile  
260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly  
275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val  
290 295 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile  
305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val  
325 330 335

Arg Leu Leu Glu Asp Gly Asp  
340

<210> 37  
<211> 343  
<212> PRT  
<213> artificial sequence

<220>  
<223> mxoxox3

<400> 37

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Ile  
1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg  
20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val  
35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe  
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala  
65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn  
85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala  
 100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly  
 115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln  
 130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn  
 145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu  
 165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asn Gly Gly Arg  
 180 185 190

Met Leu Ile His Ile Ser Arg Thr Lys Thr Leu Val Ser Thr Ala Gly  
 195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Gln Trp  
 210 215 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys  
 225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Arg Leu  
 245 250 255

Ser Thr Arg Ala Leu Gly Gly Ile Phe Glu Ala Thr His Arg Leu Ile  
 260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly  
 275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val  
 290 295 300

Ser Ile Leu Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile  
 305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val  
325 330 335

Arg Leu Leu Glu Asp Gly Asp  
340

<210> 38  
<211> 343  
<212> PRT  
<213> artificial sequence

<220>  
<223> mxoxox4

<400> 38

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val  
1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg  
20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val  
35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe  
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Cys Leu Gln Ala  
65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn  
85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala  
100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly  
115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Lys Arg Thr Asp Phe Asp Gln  
130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn  
145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu  
 165 170 175  
 Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg  
 180 185 190  
 Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly  
 195 200 205  
 Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp  
 210 215 220  
 Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys  
 225 230 235 240  
 Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu  
 245 250 255  
 Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile  
 260 265 270  
 Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Gln Ala Trp Ser Gly  
 275 280 285  
 His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val  
 290 295 300  
 Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile  
 305 310 315 320  
 Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val  
 325 330 335  
 Arg Leu Leu Glu Asp Gly Asp  
 340

<210> 39  
 <211> 343  
 <212> PRT  
 <213> artificial sequence  
  
 <220>  
 <223> mxoxox5

<400> 39

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val  
1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Ala Met Phe Arg  
20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val  
35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe  
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala  
65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn  
85 90 95

Met Leu His Arg Gln Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala  
100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly  
115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln  
130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn  
145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu  
165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg  
180 185 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly  
195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Gln Val Glu Arg Trp  
210 215 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys  
225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu  
245 250 255

Ser Thr Arg Ala Leu Gly Gly Ile Phe Glu Ala Thr His Arg Leu Ile  
260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly  
275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val  
290 295 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Ser Asn Val Asn Ile  
305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val  
325 330 335

Arg Leu Leu Glu Asp Gly Asp  
340

<210> 40  
<211> 343  
<212> PRT  
<213> artificial sequence

<220>  
<223> mxoxox6

<400> 40

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val  
1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg  
20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val  
35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe  
50 55 60



Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala  
 65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn  
 85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala  
 100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly  
 115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln  
 130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn  
 145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu  
 165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg  
 180 185 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly  
 195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp  
 210 215 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys  
 225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu  
 245 250 255

Ser Thr Arg Ala Leu Gly Gly Ile Phe Glu Ala Thr His Arg Leu Ile  
 260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Gln Ala Trp Ser Gly  
 275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val  
290 295 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Ser Asn Val Asn Ile  
305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val  
325 330 335

Arg Leu Leu Glu Asp Gly Asp  
340

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<220>  
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<223> nn is either TT, TG, GT, GG, TC, CC, or AA

<400> 41  
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13

<210> 42  
<211> 13  
<212> DNA  
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<220>  
<223> loxK2

<400> 42  
ataacaacgt ata

13

<210> 43  
<211> 13  
<212> DNA  
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<220>  
<223> loxK1

<400> 43  
atacctttgt ata

13

<210> 44  
<211> 34  
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<220>  
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<400> 44  
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34

<210> 45  
<211> 34  
<212> DNA  
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<220>  
<223> loxK2

<400> 45  
ataacaacgt atataccttt ctatagcttg ttat

34

<210> 46  
<211> 34  
<212> DNA  
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<220>  
<223> loxK1

<400> 46  
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34

<210> 47  
<211> 34  
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<220>  
<223> loxK2 'GG'

<400> 47  
ataacggcgt atataccttt ctatagcccg ttat

34

<210> 48  
<211> 34  
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<220>  
<223> loxK2 'CC'

<400> 48  
ataaccccggt atataccttt ctatagcggg ttat

34

<210> 49  
<211> 34  
<212> DNA  
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<220>  
<223> loxK2 'TC'

<400> 49  
ataactccgt atataccttt ctatagcgag ttat

34

<210> 50  
<211> 34  
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<220>  
<223> loxK2 'GT'

<400> 50  
ataacgtcgt atataccttt ctatagcacg ttat

34

<210> 51  
<211> 34  
<212> DNA  
<213> artificial sequence

<220>  
<223> loxK2 'TG'

<400> 51  
ataactgcgt atataccttt ctatagccag ttat

34

<210> 52  
<211> 34  
<212> DNA  
<213> artificial sequence

<220>  
<223> LoxP

<400> 52  
ataacttcgt ataattgtatg ctatacgaag ttat

34

<210> 53  
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<220>

<223> LoxK1

<400> 53

gagcctttgt atataccttt ctatacaaag gctt

34

<210> 54

<211> 34

<212> DNA

<213> artificial sequence

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<400> 54

gatacaacgt atataccttt ctatacgttg tatt

34

<210> 55

<211> 64

<212> DNA

<213> artificial sequence

<220>

<223> Gene

<400> 55

gctagcgaat tcgagcttcg gtacccgggg atcctctaga gtcgacctgc aggcattgcaa

60

gctt

64

<210> 56

<211> 33

<212> DNA

<213> artificial sequence

<220>

<223> oligonucleotide

<400> 56

agcttggagg ctatcatgtc gaccaagcta gca

33

<210> 57

<211> 33

<212> DNA

<213> artificial sequence

<220>

<223> oligonucleotide

<400> 57

gatctgctag cttggctcgac atgatagcct cca

33

<210> 58  
<211> 35  
<212> DNA  
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<220>  
<223> oligonucleotide

<400> 58  
gatctgatat ctgcggccgc tgacgtgact cgagt

35

<210> 59  
<211> 35  
<212> DNA  
<213> artificial sequence

<220>  
<223> oligonucleotide

<400> 59  
ctagactcga gtcacgtcag cggccgcaga tatca

35

<210> 60  
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<220>  
<223> oligonucleotide

<400> 60  
gaagttccta ttc

13

<210> 61  
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<220>  
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<400> 61  
tctagaaa

8

<210> 62  
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<220>  
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<400> 62  
gtataggaac ttc

13

<210> 63  
<211> 27  
<212> DNA  
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<220>  
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<400> 63  
gaagttccta ttccgaagtt cctattc

27

<210> 64  
<211> 6  
<212> DNA  
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<220>  
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<400> 64  
tctaga

6

<210> 65  
<211> 13  
<212> DNA  
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<220>  
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<400> 65  
gaagttcata ttc

13

<210> 66  
<211> 13  
<212> DNA  
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<220>  
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<400> 66  
gtatatgaac ttc

13

<210> 67  
<211> 13  
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<220>  
<223> oligonucleotide

<400> 67  
gaagttacta ttc

13

<210> 68  
<211> 13  
<212> DNA  
<213> artificial sequence

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<223> oligonucleotide

<400> 68  
gtatagtaac ttc

13

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